

## SEQUENCE LISTING

<110> Ziv Shani et al.

<120> PROCESS OF EXPRESSING AND ISOLATING RECOMBINANT PROTEINS AND RECOMBINANT  
PROTEIN PRODUCTS FROM PLANTS, PLANT DERIVED TISSUES OR CULTURED PLANT CELLS

<130> 20101

<150> 09/329,234

<151> June 10, 1999

<160> 26

<170> PatIn Ver. 2.1

<210> 1

<211> 4

<212> PRT

<213> unknown

<400> 1

His Asp Glu Leu

4

<210> 1

<211> 4

<212> PRT

<213> unknown

<400> 1

Lys Asp Glu Leu

4

<210> 3

<211> 150

<212> DNA

<213> Arabidopsis thaliana

<400> 3

ATGGCGCGAA AATCCCTAAT TTCCCGGTG ATTTTGCTCG CCGTTCTTCT CTTCTCTCCG 60  
CCGATTACT CCGCCGGTCA CGATTACCGC GACGCTCTCC GTAAAAGCAT TCTCTCTTC 120  
GAAGGTCAAC GTCCGGTAA ACTCCCTCCA 150

<210> 4

<211> 29

<212> DNA

<213> Artificial sequence

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&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:PCR primer

&lt;400&gt; 4

AAAAAGATCT ATGGCGCGAA AATCACTAA 29

&lt;210&gt; 5

&lt;211&gt; 29

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:PCR primer

&lt;400&gt; 5

AAAATCTAGA TTTACGGAGA GCGTCGCG 29

&lt;210&gt; 6

&lt;211&gt; 1305

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:construct

&lt;400&gt; 6

CCATGGCGGC GGTAGAAAAT AAAGAAGAAA CACCAGAAAC ACCAGAACT GATTCAGAAG 60  
AAGAAGTAAC AATCAAAGCT AACCTAATCT TTGCAAATGG AAGCACACAA ACTGCAGAAT 120  
TCAAAGGAAC ATTTGAAAAA GCAACATCAG AAGCTTATGA GTATGCAGAT ACTTTGAAGA 180  
AAGACAATGG AGAATATACT GTAGATGTTG CAGATAAAGG TTATACTTTA AATATTAAAT 240  
TTGCTGGAAG AGAAAAACA CCAGAAGAAC CAAAAGAAGA AGTTACTATT AAAGCAAAC 300  
TAATCTATGC AGATGGAAAA ACACAAACAG CAGAATTCAA AGGAACATTT GAAGAAGCAA 360  
CAGCAGAAGC ATACAGATAT GCAGATGCAT TAAAGAAGGA CAATGGAGAA TATACAGTAG 420  
ACGTTGCAGA TAAAGGTTAT ACTTTAAATA TTAAATTTGC TGGAAAAGAA AAAACACCAG 480  
AAGAACCAAA AGAAGAAGTT ACTATTAAAG CAACTTAAT CTATGCAGAT GGAAAAACAC 540  
AAACAGCAGA ATTCAAAGGA ACATTGAAG AAGCAACAGC AGAAGCATAC AGATATGCTG 600  
ACTTATTAGC AGCAAAGAA AATGGTAAAT ATACAGTAGA CGTTGCAGAT AAAGTTATA 660  
CTTTAAATAT TAAATTTGCT GGAAAAGAAA AAACACCAGA AGAACCACAA GAAGAAGTTA 720  
CTATTAAAGC AAACCTAATC TATGCAGATG GAAAACTCA AACAGCAGAG TTCAAAGGAA 780  
CATTTCAGAG AGCAACAGCA GAAGCATACA GATACGCTGA CTTATTAGCA AAAGAAATG 840  
GTAAATATAC AGCAGACTTA GAAGATGGTG GATACACTAT TAATATTAGA TTTGCAGGTA 900  
AGAAAGTTGA CGAAAACCA GAAGGGATCC CTCCGACGCC GACCCCGACT AGTGGTCCGG 960  
CCGGGTGCCA GGTGCTGTGG GCGCTCAACC AGTGAACAC CGGCTTCACC GCGAACGTCA 1020

CCGTGAAGAA CACGTCCTCC GCTCCGGTAG ACGGCTGGAC GCTCACGTTT AGCTTCCCGT 1080  
CCGGCCAGCA GGTCACCCAG GCGTGGAGCT CGACGGTCAC GCAGTCCGGC TCGGCCGTGA 1140  
CGGTCCGCAA CGCCCCGTGG AACGGCTCGA TCCCGGCGGG CGGCACCGCG CAGTTCGGCT 1200  
TCAACGGCTC GCACACGGGC ACCAACGCCG CGCCGACGGC GTTCTCGCTC AACGGCACGC 1260  
CCTGCACGGT CGGCGTCGAG CACCACCACC ACCACCACCA CCACT 1305

<210> 7

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 7

AAAATCTAGA ATGGCGGCGG TAGAAAATAA AG 32

<210> 8

<211> 43

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 8

AAAAGTCGAC TTAAAGTTCA TCATGCTCGA CGCCGACCGT GCA 43

<210> 9

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 9

AAAAACTAGT GCTAGCGGTC CAGCCGGC 28

<210> 10

<211> 43

<212> DNA

<213> Artificial sequence

<220>

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&lt;223&gt; Description of Artificial Sequence:PCR primer

&lt;400&gt; 10

AAAAGTCGAC TTAAAGTTCA TCATGTCCAA CGGTGCAAGG GGC 43

&lt;210&gt; 11

&lt;211&gt; 1418

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:construct

&lt;400&gt; 11

GGGGATCTAT GCGCGGAAAA TCCCTAATTT TCCCGGTGAT TTTGCTCGCC GTTCTTCTCT 60  
TCTCTCCGCC GATTACTCC GCGGTCACG ATTACCGCGA CGCTCTCCGT AAATCTAGAA 120  
TGGCGGCGGT AGAAAATAAA GAAGAACAC CAGAAACACC AGAACTGAT TCAGAAGAAG 180  
AAGTAACAAT CAAAGCTAAC CTAATCTTTG CAAATGGAAG CACACAACT GCAGAATTCA 240  
AAGGAACATT TGAAAAAGCA ACATCAGAAG CTTATGAGTA TGCAGATACT TTGAAGAAAG 300  
ACAATGGAGA ATATACTGTA GATGTTGCAG ATAAAGGTTA TACTTTAAAT ATTAAATTTG 360  
CTGGAAGA AAAACACCA GAAGAACCA AAGAAGAAGT TACTATTAAG GCAAACTTAA 420  
TCTATGCAGA TGGAAAAACA CAAACAGCAG AATTCAAAGG AACATTTGAA GAAGCAACAG 480  
CAGAAGCATA CAGATATGCA GATGCATTAA AGAAGGACAA TGGAGAATAT ACAGTAGACG 540  
TTGCAGATAA AGGTTATACT TTAAATATTA AATTGCTGG AAAAGAAAAA ACACCAGAAG 600  
AACCAAAAGA AGAAGTTACT ATTAAAGCAA ACTTAATCTA TGCAGATGGA AAAACACAAA 660  
CAGCAGAATT CAAAGGAACA TTTGAAGAAG CAACAGCAGA AGCATAACAG TATGCTGACT 720  
TATTAGCAGC AAAAGAAAAT GGTAAATATA CAGTAGACGT TGCAGATAAA GGTTATACTT 780  
TAAATATTAA ATTTGCTGGA AAAGAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA 840  
TTAAAGCAAA CTTAATCTAT GCAGATGGAA AACTCAAAC AGCAGAGTTC AAAGGAACAT 900  
TTGCAGAAGC AACAGCAGAA GCATACAGAT ACGCTGACTT ATTAGCAAAA GAAAATGGTA 960  
AATATACAGC AGACTTAGAA GATGGTGGAT AACTATTAA TATTAGATTT GCAGGTAAGA 1020  
AAGTTGACGA AAAACCAGAA GGGATCCCTC CGACGCCGAC CCCGACTAGT GCTAGCGGTC 1080  
CAGCCGGCTG CCAGGTTCTG TGGGGTGTTA ACCAGTGGAA CACCGGTTTC ACCGCTCAGG 1140  
TTACCGTTAA AAACACGGGC TCAGCTCCGG TTGACGGTTG GACCCTGACC TTCTCTTTTC 1200  
CCTCGGGTCA GCAGGTAAC CAGGCTTGGT CATCTACAGT TACCCAGTCT GGATCCGCTG 1260  
TTACAGTTCG TAACGCTCCG TGGAACGGTA ATATTCCTGC AGGTGGAACC GCTCAGTTCG 1320  
GTTTCCAAGG TTCTCACACC GGTACCAACG CGGCGCCAAC CGCTTTCTCT CTGAACGGGG 1380  
CCCCTTGCAC CGTTGGACAT GATGAACTTT AAGTCGAC 1418

&lt;210&gt; 12

&lt;211&gt; 467

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&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:construct translation

&lt;400&gt; 12

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Met Ala Arg Lys Ser Leu Ile Phe Pro Val Ile Leu Leu Ala Val Leu
 1           5           10           15

Leu Phe Ser Pro Pro Ile Tyr Ser Ala Gly His Asp Tyr Arg Asp Ala
          20           25           30

Leu Arg Lys Ser Arg Met Ala Ala Val Glu Asn Lys Glu Glu Thr Pro
 35           40           45

Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu Val Thr Ile Lys Ala Asn
 50           55           60

Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr Ala Glu Phe Lys Gly Thr
 65           70           75           80

Phe Glu Lys Ala Thr Ser Glu Ala Tyr Glu Tyr Ala Asp Thr Leu Lys
          85           90           95

Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr
 100           105           110

Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro Lys
 115           120           125

Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys Thr
 130           135           140

Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala
 145           150           155           160

Tyr Arg Tyr Ala Asp Ala Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val
 165           170           175

Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys
 180           185           190

Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn
 195           200           205

Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr
 210           215           220

Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala
 225           230           235           240

Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
 245           250           255

Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
 260           265           270

Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
 275           280           285

Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Ala Glu Ala Thr Ala Glu
 290           295           300

Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
 305           310           315           320

Ala Asp Leu Glu Asp Gly Gly Tyr Thr Ile Asn Ile Arg Phe Ala Gly
 325           330           335

Lys Lys Val Asp Glu Lys Pro Glu Gly Ile Pro Pro Thr Pro Thr Pro
 340           345           350

Thr Ser Ala Ser Gly Pro Ala Gly Cys Gln Val Leu Trp Gly Val Asn
 355           360           365

Gln Trp Asn Thr Gly Phe Thr Ala Gln Val Thr Val Lys Asn Thr Gly

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370	375	380
Ser Ala Pro Val Asp Gly Trp Thr Leu Thr Phe Ser Phe Pro Ser Gly		
385	390	395 400
Gln Gln Val Thr Gln Ala Trp Ser Ser Thr Val Thr Gln Ser Gly Ser		
	405	410 415
Ala Val Thr Val Arg Asn Ala Pro Trp Asn Gly Asn Ile Pro Ala Gly		
	420	425 430
Gly Thr Ala Gln Phe Gly Phe Gln Gly Ser His Thr Gly Thr Asn Ala		
	435	440 445
Ala Pro Thr Ala Phe Ser Leu Asn Gly Ala Pro Cys Thr Val Gly His		
	450	455 460
Asp Glu Leu		
465		

&lt;210&gt; 13

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:PCR primer

&lt;400&gt; 13

CTAGTCATGA TGAAC TTAA GAGCT 25

&lt;210&gt; 14

&lt;211&gt; 17

&lt;212&gt; DNA

&lt;213&gt; artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:PCR primer

&lt;400&gt; 14

CTTAAAGTTC ATCATGA 17

&lt;210&gt; 15

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:PCR primer

&lt;400&gt; 24

AAAACCCGGG ATGGCGCGAA AATC 24

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&lt;210&gt; 16

&lt;211&gt; 33

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:PCR primer

&lt;400&gt; 16

AAAAGACGTC TTACGGAGAG CGTCGCGTA ATC 33

&lt;210&gt; 17

&lt;211&gt; 1560

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:construct

&lt;400&gt; 17

GCCCCCCTC GAGCCCGGGA TGGCGCGAAA ATCCCTAATT TTCCCGGTGA TTTTGCTCGC 60  
CGTTCTTCTC TTCTCTCCGC CGATTACTC CGCCGGTCAC GATTACCGCG ACGCTCTCCG 120  
TAAGACGTCC GGTCCAGCCG GGTGCCAGGT TCTGTGGGGT GTTAACCACT GGAACACCGG 180  
TTTACCCGCT CAGGTTACCG TTAACAAACAC GGGCTCAGCT CCGGTTGACG GTTGAGCCCT 240  
GACCTTCTCT TTTCCCTCGG GTCAGCAGGT AACTCAGGCT TGGTCATCTA CAGTTACCCA 300  
GTCTGGATCC GCTGTACAG TTCGTAACGC TCCGTGGAAC GGTAATATTC CTGCAGGTGG 360  
AACCCTCTAG TTCGGTTTCC AAGGTTCTCA CACCGGTACC AACCGGGCGC CAACCGCTTT 420  
CTCTCTGAAC GGGGCCCTT GCACCGTTGG TCCGACTACC TCACCTACAA CGCGTAAGCT 480  
CTGCAGCCTG GACAACGGGG ACTGTGACCA GTTCTGCCAC GAGGAACAGA ACTCTGTGGT 540  
GTGCTCCTGC GCCCCGCGGT ACACCCTGGC TGACAACGGC AAGGCCTGCA TTCCACAGG 600  
GCCCTACCCC TGTGGGAAAC AGACCCTGGA ACGCAGGAAG AGGTCAGTG CCCAGGCCAC 660  
CAGCAGCAGC GGGGAGGCCC CTGACAGCAT CACATGGAAG CCATATGATG CAGCCGACCT 720  
GGACCCACCC GAGAACCCCT TCGACCTGCT TGACTTTGAT CAGACGCAGC CTGAGAGGGG 780  
CGACAACAAC ATTGAAGGTC GTATCGTGGG AGGCCAGGAA TGCAAGGACG GGGAGTGTC 840  
CTGGCAGGCC CTGCTCATCA ATGAGGAAAA CGAGGGTTTC TGTGGTGGAA CCATTCTGAG 900  
CGAGTTCTAC ATCCTAACGG CAGCCCCTG TCTCTACCAA GCCAAGAGAT TCAAGGTGAG 960  
GGTAGGGGAC CGGAACACGG AGCAGGAGGA GGGCGGTGAG GCGGTGCACG AGGTGGAGGT 1020  
GGTCATCAAG CACAACCGGT TCACAAAGGA GACCTATGAC TTCGACATCG CCGTGCTCCG 1080  
GCTCAAGACC CCCATCACCT TCCGCATGAA CGTGGCGCCT GCCTGCCTCC CCGAGCGTGA 1140  
CTGGGCCGAG TCCACGCTGA TGACGCAGAA GACGGGGATT GTGAGCGGCT TCGGGCGCAC 1200  
CCACGAGAAG GGCCGCGAGT CCACCAGGCT CAAGATGCTG GAGGTGCCCT ACGTGGACCG 1260

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CAACAGCTGC AAGCTGTCCA GCAGCTTCAT CATCACCAG AACATGTTCT GTGCCGGCTA 1320  
 CGACACCAAG CAGGAGGATG CCTGCCAGGG GGACAGCGGG GGCCCGCACG TCACCCGCTT 1380  
 CAAGGACACC TACTTCGTGA CAGGCATCGT CAGCTGGGGA GAGGGCTGTG CCCGTAAGGG 1440  
 GAAGTACGGG ATCTACACCA AGGTCACCGC CTTCTCAAG TGGATCGACA GGTCCATGAA 1500  
 AACCAGGGGC TTGCCAAGG CCAAGCCTAC TAGTCATGAT GAACTTTAAG AGCTCCAGCT 1560

&lt;210&gt; 18

&lt;211&gt; 509

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:construct translation

&lt;400&gt; 18

Met Ala Arg Lys Ser Leu Ile Phe Pro Val Ile Leu Leu Ala Val Leu  
 1 5 10 15  
 Leu Phe Ser Pro Pro Ile Tyr Ser Ala Gly His Asp Tyr Arg Asp Ala  
 20 25 30  
 Leu Arg Lys Thr Ser Gly Pro Ala Gly Cys Gln Val Leu Trp Gly Val  
 35 40 45  
 Asn Gln Trp Asn Thr Gly Phe Thr Ala Gln Val Thr Val Lys Asn Thr  
 50 55 60  
 Gly Ser Ala Pro Val Asp Gly Trp Thr Leu Thr Phe Ser Phe Pro Ser  
 65 70 75 80  
 Gly Gln Gln Val Thr Gln Ala Trp Ser Ser Thr Val Thr Gln Ser Gly  
 85 90 95  
 Ser Ala Val Thr Val Arg Asn Ala Pro Trp Asn Gly Asn Ile Pro Ala  
 100 105 110  
 Gly Gly Thr Ala Gln Phe Gly Phe Gln Gly Ser His Thr Gly Thr Asn  
 115 120 125  
 Ala Ala Pro Thr Ala Phe Ser Leu Asn Gly Ala Pro Cys Thr Val Gly  
 130 135 140  
 Pro Thr Thr Ser Pro Thr Thr Arg Lys Leu Cys Ser Leu Asp Asn Gly  
 145 150 155 160  
 Asp Cys Asp Gln Phe Cys His Glu Glu Gln Asn Ser Val Val Cys Ser  
 165 170 175  
 Cys Ala Arg Gly Tyr Thr Leu Ala Asp Asn Gly Lys Ala Cys Ile Pro  
 180 185 190  
 Thr Gly Pro Tyr Pro Cys Gly Lys Gln Thr Leu Glu Arg Arg Lys Arg  
 195 200 205  
 Ser Val Ala Gln Ala Thr Ser Ser Ser Gly Glu Ala Pro Asp Ser Ile  
 210 215 220  
 Thr Trp Lys Pro Tyr Asp Ala Ala Asp Leu Asp Pro Thr Glu Asn Pro  
 225 230 235 240  
 Phe Asp Leu Leu Asp Phe Asp Gln Thr Gln Pro Glu Arg Gly Asp Asn  
 245 250 255  
 Asn Ile Glu Gly Arg Ile Val Gly Gly Gln Glu Cys Lys Asp Gly Glu  
 260 265 270



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Cys Pro Trp Gln Ala Leu Leu Ile Asn Glu Glu Asn Glu Gly Phe Cys  
 275 280 285  
 Gly Gly Thr Ile Leu Ser Glu Phe Tyr Ile Leu Thr Ala Ala His Cys  
 290 295 300  
 Leu Tyr Gln Ala Lys Arg Phe Lys Val Arg Val Gly Asp Arg Asn Thr  
 305 310 315 320  
 Glu Gln Glu Glu Gly Gly Glu Ala Val His Glu Val Glu Val Val Ile  
 325 330 335  
 Lys His Asn Arg Phe Thr Lys Glu Thr Tyr Asp Phe Asp Ile Ala Val  
 340 345 350  
 Leu Arg Leu Lys Thr Pro Ile Thr Phe Arg Met Asn Val Ala Pro Ala  
 355 360 365  
 Cys Leu Pro Glu Arg Asp Trp Ala Glu Ser Thr Leu Met Thr Gln Lys  
 370 375 380  
 Thr Gly Ile Val Ser Gly Phe Gly Arg Thr His Glu Lys Gly Arg Gln  
 385 390 395 400  
 Ser Thr Arg Leu Lys Met Leu Glu Val Pro Tyr Val Asp Arg Asn Ser  
 405 410 415  
 Cys Lys Leu Ser Ser Ser Phe Ile Ile Thr Gln Asn Met Phe Cys Ala  
 420 425 430  
 Gly Tyr Asp Thr Lys Gln Glu Asp Ala Cys Gln Gly Asp Ser Gly Gly  
 435 440 445  
 Pro His Val Thr Arg Phe Lys Asp Thr Tyr Phe Val Thr Gly Ile Val  
 450 455 460  
 Ser Trp Gly Glu Gly Cys Ala Arg Lys Gly Lys Tyr Gly Ile Tyr Thr  
 465 470 475 480  
 Lys Val Thr Ala Phe Leu Lys Trp Ile Asp Arg Ser Met Lys Thr Arg  
 485 490 495  
 Gly Leu Pro Lys Ala Lys Pro Thr Ser His Asp Glu Leu  
 500 505

&lt;210&gt; 19

&lt;211&gt; 32

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:PCR primer

&lt;400&gt; 19

AAAAGACGTC GGCTAGCGGA ATAATGGTAG CG 32

&lt;210&gt; 20

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:PCR primer

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&lt;400&gt; 20

AAAAACCGGT TGGGGATGGG GTCGGAC 27

&lt;210&gt; 21

&lt;211&gt; 1860

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:construct

&lt;400&gt; 21

CCCCCCCCTC GAGCCCGGGA TGGCGCGAAA ATCCCTAATT TTCCCGGTGA TTTTGCTCGC 60  
CGTTCCTTCTC TTCTCTCCGC CGATTACTC CGCCGGTCAC GATTACCGCG ACCTCTCTCCG 120  
TAAGACGTCG GCTAGCGGAA TAATGGTAGC GACAGCAAAA TACGGAACAC CGGTCATCGA 180  
TGGAGAGATA GACGAGATCT GGAACACGAC AGAGGAGATA GAGACGAAAG CGGTGGCCAT 240  
GGGATCGCTT GACAAGAACG CGACAGCGAA AGTGAGGGTG CTGTGGGACG AGAACTACCT 300  
GTACGTACTT GCAATCGTGA AAGACCCCGT TCTGAACAAA GACAACAGCA ACCCGTGGGA 360  
ACAGGATTCC GTGGAGATCT TCATCGACGA GAACAACCAC AAGACAGGAT ACTACGAAGA 420  
CGACGACGCA CAGTTCAGGG TGAATACAT GAACGAGCAG ACCTTTGGAA CGGGAGGAAG 480  
TCCAGCGAGG TTCAAGACAG CGGTGAAACT GATCGAAGGA GGATACATAG TTGAGGCAGC 540  
GATCAAGTGG AAGACGATCA AACCACACCC GAACACGGTG ATAGGATTCA ACATCCAGGT 600  
GAACGATGCG AACGAGAAAG GGCAGAGGGT CGGTATCATC TCCTGGAGCG ATCCCAACAA 660  
CAACAGCTGG AGAGATCCTT CAAAGTTCGG TAACCTCAGG CTCATCAAGG GATCTGGTCC 720  
GACCCCATCC CCAACGCGTA AGCTCTGCAG CCTGGACAAC GGGGACTGTG ACCAGTTCTG 780  
CCACGAGGAA CAGAATCTG TGGTGTGCTC CTGCGCCCGC GGGTACACCC TGGCTGACAA 840  
CGGCAAGGCC TGCATTCCCA CAGGGCCCTA CCCCTGTGGG AAACAGACCC TGGAACGCAG 900  
GAAGAGGTCA GTGGCCCAAG CCACCAGCAG CAGCGGGGAG GCCCCTGACA GCATCACATG 960  
GAAGCCATAT GATGCAGCCG ACCTGGACCC CACCGAGAAC CCCTTCGACC TGCTTGACTT 1020  
TGATCAGACG CAGCCTGAGA GGGGCGACAA CAACATTGAA GGTCTGATCG TGGGAGGCCA 1080  
GGAATGCAAG GACGGGGAGT GTCCCTGGCA GGCCCTGCTC ATCAATGAGG AAAACGAGGG 1140  
TTTCTGTGGT GGAACCATTC TGAGCGAGTT CTACATCCTA ACGGCAGCCC ACTGTCTCTA 1200  
CCAAGCCAAG AGATTCAAGG TGAGGGTAGG GGACCGGAAC ACGGAGCAGG AGGAGGGCGG 1260  
TGAGGCGGTG CACGAGGTGG AGGTGGTCAT CAAGCACAAC CGGTTACAA AGGAGACCTA 1320  
TGACTTCGAC ATCGCCGTGC TCCGGCTCAA GACCCCATC ACCTTCGGCA TGAACGTGGC 1380  
GCCTGCTGCG CTCCCGAGC GTGACTGGGC CGAGTCCACG CTGATGACGC AGAAGACGGG 1440  
GATTGTGAGC GGCTTCGGGC GCACCCACGA GAAGGGCCGG CAGTCCACCA GGCTCAAGAT 1500  
GCTGGAGGTG CCCTACGTGG ACCGCAACAG CTGCAAGCTG TCCAGCAGCT TCATCATCAC 1560  
CCAGAACATG TTCTGTGCCG GCTACGACAC CAAGCAGGAG GATGCCTGCC AGGGGGACAG 1620  
CGGGGGCCCG CACGTCACCC GCTTCAAGGA CACCTACTTC GTGACAGGCA TCGTCAGCTG 1680

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GGGAGAGGGC TGTGCCCCGTA AGGGGAAGTA CGGGATCTAC ACCAAGGTCA CCGCCTTCCT 1740  
 CAAGTGGATC GACAGGTCCA TGAAAACCAG GGGCTTGCCC AAGGCCAAGC CTACTAGTCA 1800  
 TGATGAACCT TAAGAGCTCC AGCTTTTGTT CCCTTTAGTG AGGGTTAATT GCGCGCTTGG 1860

&lt;210&gt; 22

&lt;211&gt; 597

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:construct translation

&lt;400&gt; 22

Met Ala Arg Lys Ser Leu Ile Phe Pro Val Ile Leu Leu Ala Val Leu  
 1 5 10 15  
 Leu Phe Ser Pro Pro Ile Tyr Ser Ala Gly His Asp Tyr Arg Asp Ala  
 20 25 30  
 Leu Arg Lys Thr Ser Ala Ser Gly Ile Met Val Ala Thr Ala Lys Tyr  
 35 40 45  
 Gly Thr Pro Val Ile Asp Gly Glu Ile Asp Glu Ile Trp Asn Thr Thr  
 50 55 60  
 Glu Glu Ile Glu Thr Lys Ala Val Ala Met Gly Ser Leu Asp Lys Asn  
 65 70 75 80  
 Ala Thr Ala Lys Val Arg Val Leu Trp Asp Glu Asn Tyr Leu Tyr Val  
 85 90 95  
 Leu Ala Ile Val Lys Asp Pro Val Leu Asn Lys Asp Asn Ser Asn Pro  
 100 105 110  
 Trp Glu Gln Asp Ser Val Glu Ile Phe Ile Asp Glu Asn Asn His Lys  
 115 120 125  
 Thr Gly Tyr Tyr Glu Asp Asp Asp Ala Gln Phe Arg Val Asn Tyr Met  
 130 135 140  
 Asn Glu Gln Thr Phe Gly Thr Gly Gly Ser Pro Ala Arg Phe Lys Thr  
 145 150 155 160  
 Ala Val Lys Leu Ile Glu Gly Gly Tyr Ile Val Glu Ala Ala Ile Lys  
 165 170 175  
 Trp Lys Thr Ile Lys Pro Thr Pro Asn Thr Val Ile Gly Phe Asn Ile  
 180 185 190  
 Gln Val Asn Asp Ala Asn Glu Lys Gly Gln Arg Val Gly Ile Ile Ser  
 195 200 205  
 Trp Ser Asp Pro Thr Asn Asn Ser Trp Arg Asp Pro Ser Lys Phe Gly  
 210 215 220  
 Asn Leu Arg Leu Ile Lys Gly Ser Gly Pro Thr Pro Ser Pro Thr Arg  
 225 230 235 240  
 Lys Leu Cys Ser Leu Asp Asn Gly Asp Cys Asp Gln Phe Cys His Glu  
 245 250 255  
 Glu Gln Asn Ser Val Val Cys Ser Cys Ala Arg Gly Tyr Thr Leu Ala  
 260 265 270  
 Asp Asn Gly Lys Ala Cys Ile Pro Thr Gly Pro Tyr Pro Cys Gly Lys  
 275 280 285  
 Gln Thr Leu Glu Arg Arg Lys Arg Ser Val Ala Gln Ala Thr Ser Ser

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290	295	300
Ser Gly Glu Ala Pro Asp Ser Ile Thr Trp Lys Pro Tyr Asp Ala Ala		
305	310	315 320
Asp Leu Asp Pro Thr Glu Asn Pro Phe Asp Leu Leu Asp Phe Asp Gln		
	325	330 335
Thr Gln Pro Glu Arg Gly Asp Asn Asn Ile Glu Gly Arg Ile Val Gly		
	340	345 350
Gly Gln Glu Cys Lys Asp Gly Glu Cys Pro Trp Gln Ala Leu Leu Ile		
	355	360 365
Asn Glu Glu Asn Glu Gly Phe Cys Gly Gly Thr Ile Leu Ser Glu Phe		
	370	375 380
Tyr Ile Leu Thr Ala Ala His Cys Leu Tyr Gln Ala Lys Arg Phe Lys		
	385	390 395 400
Val Arg Val Gly Asp Arg Asn Thr Glu Gln Glu Glu Gly Gly Glu Ala		
	405	410 415
Val His Glu Val Glu Val Val Ile Lys His Asn Arg Phe Thr Lys Glu		
	420	425 430
Thr Tyr Asp Phe Asp Ile Ala Val Leu Arg Leu Lys Thr Pro Ile Thr		
	435	440 445
Phe Arg Met Asn Val Ala Pro Ala Cys Leu Pro Glu Arg Asp Trp Ala		
	450	455 460
Glu Ser Thr Leu Met Thr Gln Lys Thr Gly Ile Val Ser Gly Phe Gly		
	465	470 475 480
Arg Thr His Glu Lys Gly Arg Gln Ser Thr Arg Leu Lys Met Leu Glu		
	485	490 495
Val Pro Tyr Val Asp Arg Asn Ser Cys Lys Leu Ser Ser Ser Phe Ile		
	500	505 510
Ile Thr Gln Asn Met Phe Cys Ala Gly Tyr Asp Thr Lys Gln Glu Asp		
	515	520 525
Ala Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Arg Phe Lys Asp		
	530	535 540
Thr Tyr Phe Val Thr Gly Ile Val Ser Trp Gly Glu Gly Cys Ala Arg		
	545	550 555 560
Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Thr Ala Phe Leu Lys Trp		
	565	570 575
Ile Asp Arg Ser Met Lys Thr Arg Gly Leu Pro Lys Ala Lys Pro Thr		
	580	585 590
Ser His Asp Glu Leu		
	595	

&lt;210&gt; 23

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:PCR primer

&lt;400&gt; 23

AAAACCATGG CGGCGGTAGA AAATAAAG 28

<210> 24

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 24

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<210> 25

<211> 24

<212> DNA

<213> Artificial sequence

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<223> Description of Artificial Sequence:PCR primer

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<210> 26

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 26

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